

18. (Amended) An enzyme molecule according to claim 17, wherein in a reaction, the D-N-carbamoyl- α -amino acid can interact with amino acids corresponding to Lys at position 126, His at position 143, Glu at position 145, Arg at position 174, Arg at position 175, and Thr at position 197 of SEQ ID NO.: 1 or 2 at the active site cavity, or an active fragment thereof.

A2 19. (Amended) An enzyme molecule according to claim 17, wherein amino acids corresponding to Glu at position 46, Glu at position 145, and Cys at position 171 of SEQ ID NO.: 1 or 2 have a hydrogen bond via a water molecule at the active site cavity, or an active fragment thereof.

20. (Amended) An enzyme molecule according to claim 17, wherein the D-N-carbamoyl- α -amino acid is selected from the group consisting of D-N-carbamoyl-phenylglycine, D-N-carbamoyl-parahydroxyphenylglycine, D-N-carbamoyl-phenylalanine, D-N-carbamoyl-valine, D-N-carbamoyl-alanine, D-N-carbamoyl-cysteine, D-N-carbamoyl-aspartic acid, D-N-carbamoyl-glutamic acid, D-N-carbamoyl-glycine, D-N-carbamoyl-histidine, D-N-carbamoyl-isoleucine, D-N-carbamoyl-lysine, D-N-carbamoyl-leucine, D-N-carbamoyl-methionine, D-N-carbamoyl-asparagine, D-N-carbamoyl-proline, D-N-carbamoyl-glutamine, D-N-carbamoyl-arginine, D-N-carbamoyl-serine, D-N-carbamoyl-threonine, D-N-carbamoyl-tryptophan, and D-N-carbamoyl-tyrosine, or an active fragment thereof.

A3 22. (Amended) A method for designing decarbamylase mutants, comprising the step of designing the decarbamylase mutants having a physical property and/or a function modified based on the stereostructure of decarbamylase according to claim 14 or 16.

A4 24. (Amended) A method for designing decarbamylase mutants, comprising the steps of: preparing a crystal of an enzyme having decarbamylase activity; determining a stereostructure of the crystal by subjecting the crystal to X-ray crystallography; and designing the decarbamylase mutants having an improved physical property and/or function based on the determined stereostructure, wherein the stereostructure is a stereostructure of decarbamylase according to claim 14 or 16.

A5 26. (Amended) A method for designing decarbamylase mutants, comprising the steps of: preparing a crystal of an enzyme having decarbamylase activity; determining a stereostructure of the crystal by subjecting the crystal to X-ray crystallography; designing the decarbamylase mutants having an improved physical property and/or function based on the determined stereostructure; and producing the decarbamylase mutants, wherein the stereostructure is a stereostructure of decarbamylase according to claim 14 or 16.

A6 31. (Amended) A decarbamylase mutant obtained with a production method according to claim 26.

32. (Amended) A method for modifying a polypeptide or protein enzyme having a